

CC the complementarity determining regions (CDRs) of murine anti-IL-8
 CC antibody 6G4.2.5 (see W69309); light chain within a human 6-subgroup
 CC I light chain template. Humanised anti-IL-8 monoclonal antibodies
 CC (MABs) and variants are described for use in diagnostic applications
 CC and in the treatment of inflammatory disorders. The invention
 CC provides conjugates of an antibody fragment and a non-proteinaceous
 CC polymer, such as PEG, that have improved half-life, mean residence
 CC time, and/or clearance rate compared to non-derivatised parental
 CC antibody fragment. Also claimed are a polypeptide that is an
 CC anti-IL-8 Mab or antibody fragment comprising a light chain amino
 CC acid sequence comprising the light chain CDRs of 6G4.2.5/ILN35A, a
 CC nucleic acid encoding such a polypeptide, and a method of producing
 CC the polypeptide in host cells. The conjugates can be used for
 CC immune therapy of inflammatory disorders, e.g. psoriasis, responses
 CC associated with inflammatory bowel disease (such as Crohn's disease
 CC and ulcerative colitis), ischemic reperfusion, adult respiratory
 CC distress syndrome, dermatitis, meningitis, encephalitis, uveitis,
 CC autoimmune diseases such as rheumatoid arthritis, Sjorgen's
 CC syndrome, vasculitis, diseases involving leukocyte diapedesis,
 CC central nervous system inflammatory disorder, multiple organ injury
 CC syndrome secondary to septicemia or trauma, alcoholic hepatitis,
 CC bacterial pneumonia, antigen-antibody complex mediated diseases,
 CC inflammations of the lung, including pleurisy, alveolitis,
 CC vasculitis, pneumonia, chronic bronchitis, bronchiectasis, and
 CC cystic fibrosis. They can also be used in diagnostic applications
 CC Sequence 242 AA;

Query Match 100.0%; Score 1679; DB 1; Length 242;
 Best Local Similarity 100.0%; Pred. No. 4,36e-117;
 Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MKKNIAFLASMFVSIATNAYADIQTQSPSSLSASVGDVITTCRPSQSLVHGIGATY 60
 QY 1 MKKNIAFLASMFVSIATNAYADIQTQSPSSLSASVGDVITTCRPSQSLVHGIGATY 60
 Db 61 LHWYQKPGKAPKLLIYKVSNRFSVPSRSGSGSGTDFLTIISSLOPEDFATYCSQST 120
 QY 61 LHWYQKPGKAPKLLIYKVSNRFSVPSRSGSGSGTDFLTIISSLOPEDFATYCSQST 120
 Db 121 HVLPTFGGQTKVEIKRTVAAPSVFIPPPSDEQLKSGTASVCLLNFPYPRKQVQKVDN 180
 QY 121 HVLPTFGGQTKVEIKRTVAAPSVFIPPPSDEQLKSGTASVCLLNFPYPRKQVQKVDN 180
 Db 181 ALQSGNSQESVTEQDSKDSYSLSTLTLKADYKHKVYACEVTHOGLSSPVTKSFNRG 240
 QY 181 ALQSGNSQESVTEQDSKDSYSLSTLTLKADYKHKVYACEVTHOGLSSPVTKSFNRG 240
 241 EC 242
 241 EC 242

RESULT 2
 ID W69313 standard; Protein: 242 AA.
 AC W69313;
 DT 15-FEB-1999 (first entry)
 DE Anti-IL-8 humanised antibody 6G4V11N35A.F(ab')2.
 KW Humanised antibody; chimeric antibody; monoclonal antibody; mouse;
 KW human; Fab; interleukin-8, inflammation, immunotherapy, psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW ischaemic reperfusion; adult respiratory distress syndrome;
 KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
 KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis,
 KW leukocyte diapedesis, multiple organ injury syndrome, septicemia,
 KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
 KW vasculitis, bronchitis, bronchiectasis; cystic fibrosis; diagnosis;
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 FT Key Location/Qualifiers
 FT CDS 439..1167
 FT /*tag= a
 FT W693137200.A2.

PD 27-AUG-1999
 PF 20-FEB-1998; U03337.
 PR 22-JAN-1998; US-012116.
 PR 21-FEB-1997; US-804444.
 PA (GETH) GENENTECH INC.
 PI Hsui V, Koumenis I, Leong SR, Presta LR, Shahrokh Z,
 PI Zapata GA;
 DR WPI: 98-467563/40.
 DR N-PSDB: V44953.
 DR New conjugates of antibody fragments - having covalently attached
 PT non-proteinaceous polymer molecules, particularly polyethylene
 PI glycol, for improving the residence time in the circulation.
 PS Example K; Fig 4B-D: 328pp; English.
 CC This is the amino acid sequence of a polypeptide encoded by
 CC plasmid p6G4V11N35A.F(ab')2 (see V44953), comprising a murine-human
 CC chimeric Fab containing complementarity determining regions of
 CC murine anti-interleukin-8 (IL-8) monoclonal antibody (MAB) 6G5.2.5
 CC (see W69309-10) in a human template. Humanised anti-IL-8 MABs (see
 CC W69301-04) are described for use in diagnostic applications and in
 CC the treatment of inflammatory disorders. The invention provides
 CC conjugates of an antibody fragment and a polymer, such as PEG, that
 CC have improved half-life, mean residence time, and/or clearance rate.
 CC The conjugates can be used for immune therapy of e.g. psoriasis,
 CC responses associated with inflammatory bowel disease (such as
 CC Crohn's disease and ulcerative colitis), ischemic reperfusion,
 CC adult respiratory distress syndrome, dermatitis, meningitis,
 CC encephalitis, uveitis, autoimmune diseases such as rheumatoid
 CC arthritis, Sjorgen's syndrome, vasculitis, diseases involving
 CC leukocyte diapedesis, central nervous system inflammatory disorder,
 CC multiple organ injury syndrome secondary to septicemia or trauma,
 CC alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex
 CC mediated diseases, inflammations of the lung, including pleurisy,
 CC alveolitis, vasculitis, pneumonia, chronic bronchitis,
 CC bronchiectasis, and cystic fibrosis.
 CC Sequence 242 AA;
 Query Match 100.0%; Score 1679; DB 1; Length 242;
 Best Local Similarity 100.0%; Pred No 4,36e-117;
 Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MKKNIAFLASMFVSIATNAYADIQTQSPSSLSASVGDVITTCRPSQSLVHGIGATY 60
 QY 1 MKKNIAFLASMFVSIATNAYADIQTQSPSSLSASVGDVITTCRPSQSLVHGIGATY 60
 Db 61 LHWYQKPGKAPKLLIYKVSNRFSVPSRSGSGSGTDFLTIISSLOPEDFATYCSQST 120
 QY 61 LHWYQKPGKAPKLLIYKVSNRFSVPSRSGSGSGTDFLTIISSLOPEDFATYCSQST 120
 Db 121 HVLPTFGGQTKVEIKRTVAAPSVFIPPPSDEQLKSGTASVCLLNFPYPRKQVQKVDN 180
 QY 121 HVLPTFGGQTKVEIKRTVAAPSVFIPPPSDEQLKSGTASVCLLNFPYPRKQVQKVDN 180
 Db 181 ALQSGNSQESVTEQDSKDSYSLSTLTLKADYKHKVYACEVTHOGLSSPVTKSFNRG 240
 QY 181 ALQSGNSQESVTEQDSKDSYSLSTLTLKADYKHKVYACEVTHOGLSSPVTKSFNRG 240
 Db 241 EC 242
 QY 241 EC 242
 RESULT 3
 ID W69302 standard; Protein: 242 AA.
 AC W69302;
 DT 15-FEB-1999 (first entry)
 DE Humanised anti-IL-8 6G4V11N35E light chain.
 KW Humanised antibody; monoclonal antibody; interleukin-8;
 KW 6G4V11N35E, inflammation, immunotherapy, therapy, psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW ischaemic reperfusion; adult respiratory distress syndrome;
 KW dermatitis; meningitis, encephalitis; uveitis; autoimmune disease;
 KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
 KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;

FI 1. 23
 FI /note= "signal peptide of STII"
 FI 24. 137
 FI /note= "murine light chain variable region"
 FI 47. 162
 FI /note= "complementarity determining region 1; determined
 FI by Kabat sequence comparison"
 FI 49. 160
 FI /note= "complementarity determining region 1; determined
 FI by X-ray crystallography"
 FI 78. 184
 FI /note= "complementarity determining region 2; determined
 FI by Kabat sequence comparison"
 FI 78. 180
 FI /note= "complementarity determining region 2; determined
 FI by X-ray crystallography"
 FI 117. 125
 FI /note= "complementarity determining region 3; determined
 FI by Kabat sequence comparison"
 FI 119. 124
 FI /note= "complementarity determining region 3; determined
 FI by X-ray crystallography"
 FI 138. 1342
 FI /note= "human light chain constant region"
 FI US5677426-A.
 PD 14-OCT-1997.
 PD 01-MAR-1995. 398613.
 PD 01-MAR-1995. US-598613.
 PD 03-MAR-1994. US-205864.
 PD (GETH) GENENTECH INC.
 PD Fong S. Robert CA. Kim YJ. Leong SR.
 PD WPI. 97-511326/47.
 PD N-PDB: 1T9549.
 PD Fragments of antibody to human interleukin 8 - comprising light
 PD and/or heavy chain sequences; used to prevent, interfere with & mediated
 PD neutrophil chemotaxis
 PS Disclosure, Fig 27A-B: 63pp: English.
 CC This is a chimeric Fab 634.2.5 comprising of complementarity determining
 CC regions (CDRs) of a light chain variable region of the murine species
 CC and light chain constant region of the human immunoglobulin IgG1. This
 CC chimeric Fab is used to construct a plasmid protein which consists
 CC of murine-human variable/constant regions of both the light and heavy
 CC chains of 634.2.5 by various standard techniques. The
 CC activity and can inhibit the IL-8 binding to human neutrophils. This anti
 CC IL-8 Fab is used to prevent interleukin-8 mediated neutrophil chemotaxis
 CC which is useful in the treatment of ulcerative colitis and bacterial
 CC pneumonia. 242 AA;
 SQ Sequence 242 AA;
 Query Match 95.8%, Score 1510, IP 1, Length 242;
 Best Local Similarity 87.6%; Pred. No. 4,89e-104;
 Matches 112, Conservation 17, Mismatches 13, Indels 0, Gaps 0;
 DB 1 MKKNIAFLASVEFSIAINATIAIVMTIPLSLPVSITQASTQVSSSVVHNTY 60
 QY 1 MKKNIAFLASVEFSIAINATIAIVMTIPLSLPVSITQASTQVSSSVVHNTY 60
 DB 61 LHWYLUKPGSPKLLIYKVSNEFSVPPKESGSSGSIIFILKISVPAEDSLVFCUST 120
 QY 61 LHWYLUKPGSPKLLIYKVSNEFSVPPKESGSSGSIIFILKISVPAEDSLVFCUST 120
 DB 121 HVLIFPAGTKLELPFAVAAPVTFIPPSSESLKSSIASVWVTLNNYVFAVWVWVN 180
 QY 121 HVLIFPAGTKLELPFAVAAPVTFIPPSSESLKSSIASVWVTLNNYVFAVWVWVN 180
 DB 181 ALGSSNSVSVVSKSLIYSLSLILSLPAKTFKHWYVAIVHFNSEVSKSNEG 240
 QY 181 ALGSSNSVSVVSKSLIYSLSLILSLPAKTFKHWYVAIVHFNSEVSKSNEG 240
 DB 241 EC 242
 QY 241 EC 242

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 FI /note= "signal peptide of STII"
 FI 24. 137
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 FI 47. 162
 FI /note= "complementarity determining region 1; determined
 FI by Kabat sequence comparison"
 FI 49. 160
 FI /note= "complementarity determining region 1; determined
 FI by X-ray crystallography"
 FI 78. 184
 FI /note= "complementarity determining region 2; determined
 FI by Kabat sequence comparison"
 FI 78. 180
 FI /note= "complementarity determining region 2; determined
 FI by X-ray crystallography"
 FI 117. 125
 FI /note= "complementarity determining region 3; determined
 FI by Kabat sequence comparison"
 FI 119. 124
 FI /note= "complementarity determining region 3; determined
 FI by X-ray crystallography"
 FI 138. 1342
 FI /note= "human light chain constant region"
 FI US5677426-A.
 PD 14-OCT-1997.
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 PD 03-MAR-1994. US-205864.
 PD (GETH) GENENTECH INC.
 PD Fong S. Robert CA. Kim YJ. Leong SR.
 PD WPI. 97-511326/47.
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 PD Fragments of antibody to human interleukin 8 - comprising light
 PD and/or heavy chain sequences; used to prevent, interfere with & mediated
 PD neutrophil chemotaxis
 PS Disclosure, Fig 27A-B: 63pp: English.
 CC This is a chimeric Fab 634.2.5 comprising of complementarity determining
 CC regions (CDRs) of a light chain variable region of the murine species
 CC and light chain constant region of the human immunoglobulin IgG1. This
 CC chimeric Fab is used to construct a plasmid protein which consists
 CC of murine-human variable/constant regions of both the light and heavy
 CC chains of 634.2.5 by various standard techniques. The
 CC activity and can inhibit the IL-8 binding to human neutrophils. This anti
 CC IL-8 Fab is used to prevent interleukin-8 mediated neutrophil chemotaxis
 CC which is useful in the treatment of ulcerative colitis and bacterial
 CC pneumonia. 242 AA;
 SQ Sequence 242 AA;
 Query Match 89.9%, Score 1510; DB 1; Length 242;
 Best Local Similarity 87.6%; Pred. No. 4,89e-104;
 Matches 112, Conservation 17, Mismatches 13, Indels 0, Gaps 0;
 DB 1 MKKNIAFLASVEFSIAINATIAIVMTIPLSLPVSITQASTQVSSSVVHNTY 60
 QY 1 MKKNIAFLASVEFSIAINATIAIVMTIPLSLPVSITQASTQVSSSVVHNTY 60
 DB 61 LHWYLUKPGSPKLLIYKVSNEFSVPPKESGSSGSIIFILKISVPAEDSLVFCUST 120
 QY 61 LHWYLUKPGSPKLLIYKVSNEFSVPPKESGSSGSIIFILKISVPAEDSLVFCUST 120
 DB 121 HVLIFPAGTKLELPFAVAAPVTFIPPSSESLKSSIASVWVTLNNYVFAVWVWVN 180
 QY 121 HVLIFPAGTKLELPFAVAAPVTFIPPSSESLKSSIASVWVTLNNYVFAVWVWVN 180
 DB 181 ALGSSNSVSVVSKSLIYSLSLILSLPAKTFKHWYVAIVHFNSEVSKSNEG 240
 QY 181 ALGSSNSVSVVSKSLIYSLSLILSLPAKTFKHWYVAIVHFNSEVSKSNEG 240
 DB 241 EC 242
 QY 241 EC 242


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RESULTS 11
ID W05632 standard. Protein: 237 AA.
AC W05632.
DI 08-JUN-1999 (first entry)
DE p5130 expression cassette encoded rhumAb CD18 light chain.
KW Murine anti-CD18 antibody. Heavy chain. Humanized. Myocardial infarction.
KW Burns: thermal injury; Ischemic shock; ischaemic haemorrhagic;
KW Hemorrhagic stroke; light chain.
KW Mus musculus.
OS Synthetic.
FH Key Location/Qualifiers
FT Sig-Sequence 1..23
PN W05632.18-A1.
PD 17-DEC-1998.
PP 12-JUN-1999.
PA (GETH) GENENTECH INC.
PI Blank GS, Narindray DS, Zapata GA:
DR WPI: 99-060267/05.
DR N-PSDB: X03840.
PT New method for recovering polypeptides from cell cultures - by
PT treating with reagent and filtering to remove reagent
PS Example: Fig 4: 43pp: English
CC A method has been developed for recovering a polypeptide comprising (a)
CC exposing a composition comprising a polypeptide to a reagent which binds
CC to or modifies the polypeptide, where the reagent is immobilized on a
CC solid phase; and (b) passing the composition through a filter bearing an
CC opposite charge to the reagent so as to remove leached reagent from the
CC composition. The present invention also describes a method for modifying
CC a precursor antibody comprising a leucine zipper by exposing the
CC precursor antibody to a protease immobilized on a solid support so that
CC the protease removes the zipper. The methods can be used to purify
CC proteins from cell cultures. They are especially useful for isolating
CC antibodies. The methods overcome the problem of reagent leakage into the
CC protein as is the case in prior art immobilized modification systems. By
CC using a opposite charge filter the reagent can be excluded from the
CC sample, preventing contamination. The present sequence represents the
CC recombinant humanised anti-CD18 antibody (rhumAb CD18) light chain,
CC which is used in an example from the present invention.
SQ Sequence 237 AA:

Query Match 87.0%, Score 1461, DB 1, Length 237:
Best Local Similarity 90.9%, Pred. No. 2, 94e-100.
Matches 220, Conservative 5, Mismatches 12, Indels 5, Gaps 2.

Db 1 MKKNIAFLASMFVSIATNAYADIQMTQSPSSLSASVGRVITICRASQD----INN-Y 55
QY 1 MKKNIAFLASMFVSIATNAYADIQMTQSPSSLSASVGRVITICRASQDVFATYYCQGN 60
Db 56 LNWYQKPKAPKLLIYVSTLHSGVPSFSGSGSDYTLTISSLPQEDFATYYCQGN 115
QY 61 LHWYQKPKAPKLLIYKVSNPFSGVPSFSGSGSDYTLTISSLPQEDFATYYCQST 120
Db 116 TLPTFGQGTKEIKTVAAAPSVFIPPSDEQLKSGTASVCLLNFPYPAKQVQKVDN 175
QY 121 HVLPTFGQGTKEIKTVAAAPSVFIPPSDEQLKSGTASVCLLNFPYPAKQVQKVDN 180
Db 176 ALQSGNSQESVTEQSDKSTYLSLTIILSKADYKHKVYACEVTHQGLSSPVTKSNRG 235
QY 181 ALQSGNSQESVTEQSDKSTYLSLTIILSKADYKHKVYACEVTHQGLSSPVTKSNRG 240
Db 236 EC 237
QY 241 EC 242

RESULTS 13
ID W0703 standard. Protein: 237 AA.
AC W0703.
DI 27-JAN-1999 (first entry)
DE Protein encoded by Fab-display antibody vector phMB4-19-1-6.
KW Murine humanised antibody; VEGF-induced angiogenesis; tumour.
KW Anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
KW retinal disorder, age-related macular degeneration, diabetic retinopathy;
KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
OS Synthetic.
FH Key Location/Qualifiers
FT Sig-Sequence 1..23
PN W0703.1-A2.
PD 15-OCT-1998.
PP 03-APR-1999.
PA (GETH) GENENTECH INC.
PI Baca M, Chen YM, Lowman HB, Presta LG, Wells JA:
DR WPI: 98-568337/48.

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18 New humanised antibody with affinity for vascular endothelial growth
 19 factor for treatment of tumours, retinal disease and other
 20 angiogenic diseases, also related nucleic acid, vectors and
 21 transgenic cells
 22 Example of Fig 5A-E is in Fig. English.
 23 The present sequence is created by the Fab display antibody vector
 24 pM84 1.7.92, which is used in the course of the invention. The
 25 specification describes humanised murine anti vascular endothelial
 26 growth factor (angi-VEGF) antibodies. The humanised antibodies
 27 are used to inhibit VEGF induced angiogenesis, particularly for treating
 28 of preventing tumours (of any type) and retinal disorders (e.g. age-
 29 related macular degeneration, diabetic retinopathy, they can also be
 30 used to treat other conditions that involve angiogenesis, e.g. rheumatoid
 31 arthritis, psoriasis, arteriosclerosis, Grave's disease, etc.
 32 Sequence 237 AA

Query Match: 86.4% Score 1451: DB 1: Length 237:
 33 Best Local Similarity 90.1%: Pred. NO. 1.73e 99:
 34 Gaps 218: Conservative 8: Mismatches 10: Indels 5: Gaps 4:

1 MKKNIALLSMVFSTAYAYALDICTSPSSLSASVGRVTIIC-SA-S-QDI-SNY 55
 2
 3 1 MKKNIALLSMVFSTAYAYALDICTSPSSLSASVGRVTIIC-SQSLVHGIGAY 60
 4
 5 56 LNWYKPKAKKLLVYASFLYSGVSPSSLSASVGRVTIIC-SQSLVHGIGAY 115
 6
 7 61 LNWYKPKAKKLLVYASFLYSGVSPSSLSASVGRVTIIC-SQSLVHGIGAY 120
 8
 9 176 ALGSSNSQSVTEDESKSTYSLSLILSKATYKHKVYATVTHAGLSSPVTSKSNPG 175
 10
 11 181 ALGSSNSQSVTEDESKSTYSLSLILSKATYKHKVYATVTHAGLSSPVTSKSNPG 240
 12
 13 236 EC 237
 14 II
 15 241 EC 242

RESULT 14
 16 E24947 standard: Protein: 237 AA.
 17 R24047:
 18 DT 08-MAR-1999 (first entry)
 19 415 Fab molecule expressed on a phagemid surface.
 20 Human: growth hormone; hGH; phagemid particle: enzyme substrate:
 21 fusion gene: phage protein coat.
 22 Homo sapiens.
 23 Synthetic.
 24 US5846765-A.
 25 PD 08-DEC-1998.
 26 PF 15-MAY-1995: 441871.
 27 PR 03-DEC-1993: US-161692.
 28 PR 03-DEC-1990: US-621667.
 29 PR 10-APR-1991: US-683400.
 30 PR 14-JUN-1991: US-715300.
 31 PR 09-AUG-1991: US-743614.
 32 PR 03-DEC-1991: WO-009133.
 33 PR 26-APR-1993: US-864452.
 34 PR 30-APR-1993: US-050058.
 35 PR 27-APR-1993: US-819928.
 36 PR 16-MAY-1995: US-441871.
 37 (GETH) GENENTECH INC.
 38 PI Matthews DJ, Wells JA, Zoller MJ:
 39 W0204690-A.
 40 11 JUN 1992.
 41 4 DECEMBER 1992.
 42 3 DECEMBER 1992: US-621667.
 43 3 DECEMBER 1992: US-683400.
 44 14 JUN 1991: US-715300.
 45 09 APR 1991: US-743614.
 46 (GETH) GENENTECH INC.
 47 Bass SA, Ballard DJ, Greene F, Brenner DJ, Lowman HB:
 48 Matthews DJ, Wells JA:
 49 W0204690-A.
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 104 14 JUN 1991: US-715300.
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 118 Matthews DJ, Wells JA:
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 151 4 DECEMBER 1992.
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 199 W0204690-A.
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 201 4 DECEMBER 1992.
 202 3 DECEMBER 1992: US-621667.
 203 3 DECEMBER 1992: US-683400.
 204 14 JUN 1991: US-715300.
 205 09 APR 1991: US-743614.
 206 (GETH) GENENTECH INC.
 207 Bass SA, Ballard DJ, Greene F, Brenner DJ, Lowman HB:
 208 Matthews DJ, Wells JA:
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 210 11 JUN 1992.
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 528 Matthews DJ, Wells JA:
 529 W0204690-A.
 530 11 JUN 1992.
 531 4 DECEMBER 1992.
 532 3 DECEMBER 1992: US-

CC the affinity molecule has affinity for the amino acid residue having the
CC modified covalent bond, and (h) separating the phagemid particles that
CC bind to the affinity molecule from those that do not bind. The selection
CC method is used for identifying enzyme substrates. The present sequence
CC represents an 4DS Fab molecule expressed on a phagemid surface from the
CC present invention.
SQ Sequence 598 AA:

Query Match: 85.84, Score 1440, DB 1, Length 698:
Res: Query Similarity 90.14, Prod No. 1 220-98
Matches 218; Conservative 5; Mismatches 14; Indels 5; Gaps 3;
DB 1 MKKNIAFLASMEVFSIATNAYADTQMTQSPSSISASVGDPTTITCRASQD-VN-TAVA- 57
QY 1 MKKNIAFLASMEVFSIATNAYADTQMTQSPSSISASVGDPTTITCRASQD-VN-TAVA- 57
DB 58 --WYCKPKAKPKLLIYSASFLYSVPSFSSPSSTGTFILTISSLOPEDFATYYCOOHY 115
QY 58 --WYCKPKAKPKLLIYSASFLYSVPSFSSPSSTGTFILTISSLOPEDFATYYCOOHY 115
DB 61 LHWYQKPKAKPKLLIYKVSNEFSGVPSFSGSGGTDFTLTISSLOPEDFATYYCSQT 120
QY 61 LHWYQKPKAKPKLLIYKVSNEFSGVPSFSGSGGTDFTLTISSLOPEDFATYYCSQT 120
DB 116 TTPPIFGQGTIVFKFTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDN 175
QY 116 TTPPIFGQGTIVFKFTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDN 175
DB 121 HYPPIFGQGTIVFKFTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDN 180
QY 121 HYPPIFGQGTIVFKFTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDN 180
DB 176 ALQSGNSQSVTELSKSTISLSLLILSKADYKHKVACEVTHQGLSSPVTKSFNPG 235
QY 176 ALQSGNSQSVTELSKSTISLSLLILSKADYKHKVACEVTHQGLSSPVTKSFNPG 235
DB 191 ALQSGNSQSVTELSKSTISLSLLILSKADYKHKVACEVTHQGLSSPVTKSFNPG 240
QY 191 ALQSGNSQSVTELSKSTISLSLLILSKADYKHKVACEVTHQGLSSPVTKSFNPG 240
DB 236 EC 237
QY 236 EC 237
DB 241 EC 242
QY 241 EC 242

Search completed. Thu May 18 11:45:07 2000
Job time : 19 secs.

CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Genentech, Inc
 CC STREET: 460 Point San Bruno Blvd
 CC CITY: South San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94080
 CC
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: WinPatIn (Genentech)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/463,587A
 CC FILING DATE: 05-Jun-1995
 CC CLASSIFICATION: 435
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: 08/050058
 CC FILING DATE: 30-APR-1993
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US91/09133
 CC FILING DATE: 03-DEC-1991
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: 07/743614
 CC FILING DATE: 09-AUG-1991
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: 07/715300
 CC FILING DATE: 14-JUN-1991
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: 07/683400
 CC FILING DATE: 10-APR-1991
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: 07/621667
 CC FILING DATE: 03-DEC-1990
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Schwartz, Timothy R.
 CC REGISTRATION NUMBER: 33171
 CC REFERENCE/DOCKET NUMBER: F0645F4D2
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415/225-7467
 CC TELEFAX: 415/952-9881
 CC TELEX: 910/371-7168
 CC INFORMATION FOR SEQ ID NO: 25:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 237 amino acids
 CC TYPE: Amino Acid
 CC TOPOLOGY: Linear
 CC
 CC SEQUENCE 237 AA; 25977 MW; 322792 CN;

Query Match 85.8%; Score 1440; DB 2; Length 237;
 Best Local Similarity 90.1%; Pred. No. 4, 88e-92;
 Matches 218; Conservative 5; Mismatches 14; Indels 5; Gaps 3;

Db 1 MKKNIAFLASMFVSIATNAYADIQMTQSPSSLSASVGDPRVITITPASQD-VN-TAVA- 57
 QY 1 MKKNIAFLASMFVSIATNAYADIQMTQSPSSLSASVGDPRVITITPASQD-VN-TAVA- 60
 Db 58 --WYQKPKGKAPKLLIYKVSNEPFSVSGSGDFTLTITSSIQPEFATYVQGHY 115
 QY 61 LHWYQKPKGKAPKLLIYKVSNEPFSVSGSGDFTLTITSSIQPEFATYVQGHY 120
 Db 115 TTPFTSQGKTKVEIKPIVAAPSEVIFPPSDEQLKSGTASVGVTLNFPYPAKQVQKVDN 175
 QY 121 HVPITFQQTQKVEIKPIVAAPSEVIFPPSDEQLKSGTASVGVTLNFPYPAKQVQKVDN 180
 Db 175 ALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTYKSNRG 235
 QY 181 ALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTYKSNRG 240
 Db 236 EC 237
 QY 241 EC 242

RESULT 6
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 AC XXXXXX
 XX
 DT
 XX
 Sequence 26, Application PC/TUS9109133
 DE XX
 DE MEDIUM TYPE: 3.5 inch, 360 Kb floppy disk
 CC
 CC GENERAL INFORMATION:
 CC APPLICANT: Genentech, Inc.
 CC APPLICANT: Garrard, Lisa J.
 CC APPLICANT: Henner, Dennis J.
 CC APPLICANT: Bass, Steven
 CC APPLICANT: Greene, Ronald
 CC APPLICANT: Lowman, Henry B.
 CC APPLICANT: Wells, James A.
 CC APPLICANT: Matthews, David J.
 CC TITLE OF INVENTION: Enrichment Method For Variant Proteins
 CC TITLE OF INVENTION: With Altered Binding Properties
 CC NUMBER OF SEQUENCES: 27
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Genentech, Inc.
 CC STREET: 460 Point San Bruno Blvd
 CC CITY: South San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94080
 CC
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: patin (Genentech)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US91/09133
 CC FILING DATE: 19911203
 CC CLASSIFICATION: 425
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: 07/743614
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: 07/715300
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: 07/683400
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: 07/621667
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Benson, Robert H.
 CC REGISTRATION NUMBER: 30,446
 CC REFERENCE/DOCKET NUMBER: 645P4
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415/266-1489
 CC TELEFAX: 415/952-9881
 CC TELEX: 910/371-7168
 CC INFORMATION FOR SEQ ID NO: 26:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 237 amino acids
 CC TYPE: AMINO ACID
 CC TOPOLOGY: linear
 CC
 CC SEQUENCE 237 AA; 25977 MW; 322792 CN;

Query Match 85.8%; Score 1440; DB 3; Length 237;
 Best Local Similarity 90.1%; Pred. No. 4, 88e-92;
 Matches 218; Conservative 5; Mismatches 14; Indels 5; Gaps 3;

Db 1 MKKNIAFLASMFVSIATNAYADIQMTQSPSSLSASVGDPRVITITPASQD-VN-TAVA- 57
 QY 1 MKKNIAFLASMFVSIATNAYADIQMTQSPSSLSASVGDPRVITITPASQD-VN-TAVA- 60
 Db 58 --WYQKPKGKAPKLLIYKVSNEPFSVSGSGDFTLTITSSIQPEFATYVQGHY 115
 QY 61 LHWYQKPKGKAPKLLIYKVSNEPFSVSGSGDFTLTITSSIQPEFATYVQGHY 120

CC REFERENCE/POCKET NUMBER: P1123
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 650/225-1489
 CC TELEFAX: 650/225-1489
 CC INFORMATION FOR SEQ ID NO: 17:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 218 amino acids
 CC TYPE: Amino Acid
 CC TOPOLOGY: Linear
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:
 Query Match: 80.1%, Score 1345; DB 2; Length 218;
 Best Local Similarity 90.9%; Pred. No. 3,07e-85;
 Matches 199; Conservative 5; Mismatches 14; Indels 1; Gaps 1;
 Db 1 DIQLTQSPSSLSASVGRVTITCPASRP-VQEGSDSYLNWYCKPKAPKLLIYAASYL 59
 24 DIQLTQSPSSLSASVGRVTITCPASRP-SLVHSGISATILHWYCKPKAPKLLIYVSNPF 83
 60 SVPSPSSSSSSSSTDTLTLSQPEFAIYVCSQSHEDPYTFGGTKVETVAAPSV 119
 84 SVPSPSSSSSSSSTDTLTLSQPEFAIYVCSQSHEDPYTFGGTKVETVAAPSV 143
 120 FIFPSEGLKSTASVLLNNFYFPAKVWKVGNALSGNSQSVTEQDSKSTYSL 179
 144 FIFPSEGLKSTASVLLNNFYFPAKVWKVGNALSGNSQSVTEQDSKSTYSL 203
 180 SSTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 218
 204 SSTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 242
 RESULT 10
 ID US-09-987-352B-24 STANDARD PFT: 218 AA.
 XX XXXXXX
 AC
 DT
 XX
 DE Sequence 19, Application US/08887352B
 CC Sequence 19, Application US/08887352B
 CC Patent No. 5994511
 CC GENERAL INFORMATION:
 CC APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 CC TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
 CC TITLE OF INVENTION: Improving Polypeptides
 CC NUMBER OF SEQUENCES: 26
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESS: Genentech, Inc.
 CC STREET: 1 DNA Way
 CC CITY: South San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94080
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: WinPatIn (Genentech)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/09/047,302P
 CC FILING DATE: 03-Jul-1997
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Svoboda, Craig G.
 CC REGISTRATION NUMBER: 39,044
 CC REFERENCE/POCKET NUMBER: P1123
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 650/225-1489
 CC TELEFAX: 650/225-1489
 CC INFORMATION FOR SEQ ID NO: 19:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 218 amino acids
 CC TYPE: Amino Acid
 CC TOPOLOGY: Linear
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:
 Query Match: 80.1%, Score 1345; DB 2; Length 218;
 Best Local Similarity 90.9%; Pred. No. 3,07e-85;
 Matches 199; Conservative 5; Mismatches 14; Indels 1; Gaps 1;
 Db 1 DIQLTQSPSSLSASVGRVTITCPASRP-VQEGSDSYLNWYCKPKAPKLLIYAASYL 59
 24 DIQLTQSPSSLSASVGRVTITCPASRP-SLVHSGISATILHWYCKPKAPKLLIYVSNPF 83
 60 SVPSPSSSSSSSSTDTLTLSQPEFAIYVCSQSHEDPYTFGGTKVETVAAPSV 119
 84 SVPSPSSSSSSSSTDTLTLSQPEFAIYVCSQSHEDPYTFGGTKVETVAAPSV 143
 120 FIFPSEGLKSTASVLLNNFYFPAKVWKVGNALSGNSQSVTEQDSKSTYSL 179
 144 FIFPSEGLKSTASVLLNNFYFPAKVWKVGNALSGNSQSVTEQDSKSTYSL 203
 180 SSTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 218
 204 SSTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 242
 RESULT 9
 ID US-09-987-352B-19 STANDARD PFT: 218 AA.
 XX XXXXXX
 AC
 DT
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 DE Sequence 19, Application US/08887352B
 CC Sequence 19, Application US/08887352B
 CC Patent No. 5994511
 CC GENERAL INFORMATION:
 CC APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 CC TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
 CC TITLE OF INVENTION: Improving Polypeptides
 CC NUMBER OF SEQUENCES: 26
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESS: Genentech, Inc.
 CC STREET: 1 DNA Way
 CC CITY: South San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94080
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: WinPatIn (Genentech)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/09/047,302P
 CC FILING DATE: 03-Jul-1997
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Svoboda, Craig G.
 CC REGISTRATION NUMBER: 39,044
 CC REFERENCE/POCKET NUMBER: P1123
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 650/225-1489
 CC TELEFAX: 650/225-1489
 CC INFORMATION FOR SEQ ID NO: 19:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 218 amino acids
 CC TYPE: Amino Acid
 CC TOPOLOGY: Linear
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:
 Query Match: 80.1%, Score 1345; DB 2; Length 218;

CC LENGTH: 218 amino acids
 CC TYPE: Amino Acid
 CC TOPOLOGY: Linear
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:
 Query Match: 80.1%, Score 1345; DB 2; Length 218;
 Best Local Similarity 90.9%; Pred. No. 3,07e-85;
 Matches 199; Conservative 5; Mismatches 14; Indels 1; Gaps 1;
 Db 1 DIQLTQSPSSLSASVGRVTITCPASRP-VQEGSDSYLNWYCKPKAPKLLIYAASYL 59
 24 DIQLTQSPSSLSASVGRVTITCPASRP-SLVHSGISATILHWYCKPKAPKLLIYVSNPF 83
 60 SVPSPSSSSSSSSTDTLTLSQPEFAIYVCSQSHEDPYTFGGTKVETVAAPSV 119
 84 SVPSPSSSSSSSSTDTLTLSQPEFAIYVCSQSHEDPYTFGGTKVETVAAPSV 143
 120 FIFPSEGLKSTASVLLNNFYFPAKVWKVGNALSGNSQSVTEQDSKSTYSL 179
 144 FIFPSEGLKSTASVLLNNFYFPAKVWKVGNALSGNSQSVTEQDSKSTYSL 203
 180 SSTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 218
 204 SSTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 242
 RESULT 10
 ID US-09-987-352B-24 STANDARD PFT: 218 AA.
 XX XXXXXX
 AC
 DT
 XX
 DE Sequence 24, Application US/08887352B
 CC Sequence 24, Application US/08887352B
 CC Patent No. 5994511
 CC GENERAL INFORMATION:
 CC APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 CC TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
 CC TITLE OF INVENTION: Improving Polypeptides
 CC NUMBER OF SEQUENCES: 26
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESS: Genentech, Inc.
 CC STREET: 1 DNA Way
 CC CITY: South San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94080
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: WinPatIn (Genentech)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/887,352B
 CC FILING DATE: 03-Jul-1997
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Svoboda, Craig G.
 CC REGISTRATION NUMBER: 39,044
 CC REFERENCE/POCKET NUMBER: P1123
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 650/225-1489
 CC TELEFAX: 650/225-1489
 CC INFORMATION FOR SEQ ID NO: 24
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 218 amino acids
 CC TYPE: Amino Acid
 CC TOPOLOGY: Linear
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:
 Query Match: 80.1%, Score 1345; DB 2; Length 218;



 W E I G H T

 (MW)

Blanco, J. A. John F. Collins, Biocompare Research Unit,
 University of Pittsburgh, University of Pittsburgh, U.K.
 Distribution rights by Oxford Molecular Ltd
 Human IgG1 protein protein database search, using Smith-Waterman algorithm
 on The May 18 11:44:05 2000, 536 new William G-11 updates/sec.
 Similar output not generated.

US-09-234-182A-56
 Description: (1-242) from US09234182A.pop
 1679
 Sequences: 1 MKNHAPLASVYRVSATIN
 Reading frame: HAM 160
 Gap 11
 Searched: 142500 seqs, 4712456 residues

Post processing: Minimum Match 98
 Listing first 45 summaries
 Summary: 16162
 16162 seqs 12 seqs 48164
 Mean 17.54, Variance 115.08, s.d. 0.356

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed.
 and is derived by analysis of the total score distribution.

Seq. No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1842	201	215	2	21624	Ig kappa chain N102	4.20e-177
2	1824	200	215	2	21624	Ig kappa chain N102 F	8.10e-175
3	1842	200	215	2	21624	Ig kappa chain N102 F	8.10e-175
4	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
5	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
6	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
7	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
8	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
9	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
10	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
11	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
12	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
13	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
14	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
15	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
16	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
17	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
18	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
19	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
20	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
21	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
22	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
23	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
24	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
25	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
26	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
27	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
28	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
29	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
30	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
31	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
32	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
33	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
34	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
35	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
36	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
37	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
38	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
39	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
40	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
41	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
42	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
43	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
44	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161
45	1842	200	215	2	21624	Ig kappa chain V111	3.46e-161

24 800 47 6 136 2 520594
 25 769 44 7 137 2 520594
 26 745 44 7 137 2 520594
 27 721 42 3 138 2 520594
 28 690 41 3 138 2 520594
 29 676 40 3 138 2 520594
 30 666 39 7 139 2 520594
 31 654 38 7 139 2 520594
 32 634 38 7 139 2 520594
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 34 631 37 6 131 2 520594
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 36 630 37 5 131 2 520594
 37 620 37 3 131 2 520594
 38 625 37 3 131 2 520594
 39 624 37 2 131 2 520594
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 41 620 37 0 131 2 520594
 42 620 36 9 131 2 520594
 43 618 36 8 131 2 520594
 44 614 36 4 131 2 520594
 45 617 36 7 131 2 520594

ALIGNMENTS

RESULT 1
 ENTRY JE0242 #type complete
 TITLE Ig kappa chain N102 precursor - human
 ORGANISM Homo sapiens #common_name man
 DATE 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
 ACCESSIONS JE0242
 REFERENCE JE0241
 #authors Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, T.; Shinoda, T.
 #submission Submitted to JIPID, November 1998
 #description Structure relationship of kappa-type light chains with AL amyloidosis. Multiple deletions found in a VKIV protein.
 #accession JE0242
 #molecule_type protein
 #residues 1-215 #label ALI
 SUMMARY #length 215 #molecular_weight 23kD #booksum 9963
 Query Match 73.4% score 1342 PR 21 fourth 215;
 Best Local Similarity 81.5% Pred. No. 4.20e-175;
 Matches 180; Conservative 15; Mismatches 20; Indels 4; Gaps 2;

1 EVLVISPGSLSPGERALSSGAS V...SNRYLAWYKPKSQAPSLDITVASSRA 56
 24 EVLVISPGSLSPGERALSSGAS V...SNRYLAWYKPKSQAPSLDITVASSRA 56
 57 EVLVISPGSLSPGERALSSGAS V...SNRYLAWYKPKSQAPSLDITVASSRA 56
 84 EVLVISPGSLSPGERALSSGAS V...SNRYLAWYKPKSQAPSLDITVASSRA 56
 117 EVLVISPGSLSPGERALSSGAS V...SNRYLAWYKPKSQAPSLDITVASSRA 56
 144 EVLVISPGSLSPGERALSSGAS V...SNRYLAWYKPKSQAPSLDITVASSRA 56
 177 EVLVISPGSLSPGERALSSGAS V...SNRYLAWYKPKSQAPSLDITVASSRA 56
 204 EVLVISPGSLSPGERALSSGAS V...SNRYLAWYKPKSQAPSLDITVASSRA 56

RESULT 2
 ENTRY JE0244 #type complete
 TITLE Ig kappa chain N102 precursor - human
 ORGANISM Homo sapiens #common_name man
 DATE 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
 ACCESSIONS JE0244
 REFERENCE JE0243

```

#authors      Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata,
               F.; Yanaki, S.; Kazi, H.; Takashi, I.; Shinoda, I.
#submission   submitted to JIPID, November 1998
#description   A new subgroup of k type light chains (VkV) identified in
               cases of AL amyloidosis.
#accession    JE0243
#molecule_type protein
#residues     1-215 #label ALI
SUMMARY       #length 215 #molecular-weight 23463 #checksum 78

Query Match    72.9%, Score 1224; DB 2; Length 215;
Best Local Similarity 82.3%; Pred. No. 9,10e-175;
Matches 181; Conservative 17; Mismatches 16; Indels 6; Gaps 4;

Db 1 EVLVTQSPATLSVSPGERATLS--VH---SN-LAWYQOKPGQAPRLIIYDASTPA 55
QY 24 DIQMTQSPSSLSASVGDRTVITCRSSQSLVHGIGATYLVHWYQOKPGKAPKLLIYKVSNEF 83
56 IGIPAFSSGSGSDTFLTISSLSQELFALYYCQYNTWPLTFGSGTKVEIKRTVAAPS 115
84 SGVPSRFSGSGSDTFLTISSLSQELFALYYCQYNTWPLTFGSGTKVEIKRTVAAPS 142
115 VFIPPSDEVLKSGIASVAVLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSDTYS 175
143 VFIPPSDEVLKSGIASVAVLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSDTYS 202
175 LSSTLTLSKADYEKKHVVACEVTHQGLSSPVTKSNPQEC 215
202 LSSTLTLSKADYEKKHVVACEVTHQGLSSPVTKSNPQEC 242

RESULT 3
ENTRY    JE0243 #type complete
TITLE    Ig kappa chain N193 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change
05-Dec-1998

ACCESSIONS
REFERENCE JE0243
#authors  Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata,
           F.; Yanaki, S.; Kazi, H.; Takashi, I.; Shinoda, I.
#submission submitted to JIPID, November 1998
#description A new subgroup of k type light chains (VkV) identified in
           cases of AL amyloidosis.
#accession JE0243
#molecule_type protein
#residues 1-215 #label ALI
SUMMARY #length 215 #molecular-weight 23455 #checksum 947

Query Match    70.4%, Score 1182; DB 2; Length 215;
Best Local Similarity 81.4%; Pred. No. 8,30e-168;
Matches 179; Conservative 15; Mismatches 20; Indels 6; Gaps 3;

Db 1 EIVMTQSPATLSVSPGERATLS--V----ATNVWVWQKUGQAPRLIIYDASTPA 55
QY 24 DIQMTQSPSSLSASVGDRTVITCRSSQSLVHGIGATYLVHWYQOKPGKAPKLLIYKVSNEF 83
56 IGIPAFSSGSGSDTFLTISSLSQELFALYYCQYNTWPLTFGSGTKVEIKRTVAAPS 115
84 SGVPSRFSGSGSDTFLTISSLSQELFALYYCQYNTWPLTFGSGTKVEIKRTVAAPS 142
115 VFIPPSDEVLKSGIASVAVLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSDTYS 175
143 VFIPPSDEVLKSGIASVAVLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSDTYS 202
175 LSSTLTLSKADYEKKHVVACEVTHQGLSSPVTKSNPQEC 215
202 LSSTLTLSKADYEKKHVVACEVTHQGLSSPVTKSNPQEC 242

RESULT 4
ENTRY    A23746 #type complete
TITLE    Ig kappa chain V-III (KAP cold agglutinin) - human

```

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#formal_name Homo sapiens #common_name man
#sequence_revision 30-Dec-1991 #text_change
16-Aug-1996
ACCESSIONS
REFERENCE A23746
#authors  Leonil, J.; Ghiso, J.; Goni, F.; Frangione, B.
           J. Biol. Chem. (1991) 266:2836-2842
#journal  The primary structure of the Fab fragment of protein KAP, a
           monoclonal immunoglobulin M cold agglutinin.
#cross-references MUID:91131575
#accession A23746 Preliminary
#status     1-215 #label LEO
#molecule_type protein
#residues   1-215 #label LEO
KEYWORDS    heterotrimer; immunoglobulin
SUMMARY     #length 215 #molecular-weight 23050 #checksum 116

Query Match    68.0%, Score 1142; DB 2; Length 215;
Best Local Similarity 78.9%; Pred. No. 3,46e-161;
Matches 172; Conservative 19; Mismatches 23; Indels 4; Gaps 2;

Db 1 EIVLTQSPATLSVSPGERATLS--GGAS--QSVSSNTLAWYQOKPGQAPRLIIYDASSRA 56
QY 24 DIQMTQSPSSLSASVGDRTVITCRSSQSLVHGIGATYLVHWYQOKPGKAPKLLIYKVSNEF 83
57 TGIPDFSGSGSDTFLTISSLEPEDFAYVYQYQSSPLTFGGGKVEIKRTVAAPS 116
84 SGVPSRFSGSGSDTFLTISSLEPEDFAYVYQYQSSPLTFGGGKVEIKRTVAAPS 143
117 FIFPPSDEQLKSGTASVVGLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSDTYS 176
144 FIFPPSDEQLKSGTASVVGLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSDTYS 203
177 SSTLTLSKADYEKKHVVAGEVTHQGLSSPVTKSNRGE 214
204 SSTLTLSKADYEKKHVVAGEVTHQGLSSPVTKSNRGE 241

RESULT 5
ENTRY    JE0241 #type complete
TITLE    Ig kappa chain Am37 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change
05-Dec-1998

ACCESSIONS
REFERENCE JE0241
#authors  Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima,
           M.; Takashi, I.; Shinoda, I.
#submission submitted to JIPID, November 1998
#description Structure relationship of kappa type light chains with AL
           amyloidosis: Multiple deletions found in a VkV protein.
#accession JE0241
#molecule_type protein
#residues 1-216 #label ALI
SUMMARY #length 216 #molecular-weight 23926 #checksum 4962

Query Match    67.3%, Score 1130; DB 2; Length 216;
Best Local Similarity 77.2%; Pred. No. 3,33e-159;
Matches 169; Conservative 15; Mismatches 32; Indels 3; Gaps 3;

Db 1 DIVLTQSPDFLAVSLGERATINCKSSQSVLYN-SKNFLAWYQOKPGQ-PKLLIW-ANVRE 57
QY 24 DIQMTQSPSSLSASVGDRTVITCRSSQSLVHGIGATYLVHWYQOKPGKAPKLLIYKVSNEF 83
58 SGVPSRFSGSGSDTFLTISSLSQELFALYYCQYNTWPLTFGSGTKVEIKRTVAAPS 117
84 SGVPSRFSGSGSDTFLTISSLSQELFALYYCQYNTWPLTFGSGTKVEIKRTVAAPS 143
118 FIFPPSDEQLKSGTASVVGLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSDTYS 177
144 FIFPPSDEQLKSGTASVVGLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSDTYS 203
178 SSTLTLSKADYEKKHVVAGEVTHQGLSSPVTKSNPQEC 216

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CC the complementarity determining regions (CDRs) of murine anti-IL-8
CC antibody 634.2.5 (see W69309) light chain within a human 6-sukgroup
CC 1 light chain template. Humanised anti-IL-8 monoclonal antibodies
CC (WABs) and variants are described for use in diagnostic applications
CC and in the treatment of inflammatory disorders. The invention
CC provides conjugates of an antibody fragment and a non-proteinaceous
CC polymer, such as PEG, that have improved half-life, mean residence
CC time, and/or clearance rate compared to non-derivatised parental
CC antibody fragment. Also claimed are a polypeptide that is an
CC anti-IL-8 MAb or antibody fragment comprising a light chain amino
CC acid sequence comprising the light chain CDRs of 664V11M35E, a
CC nucleic acid encoding such a polypeptide, and a method of producing
CC the polypeptide in host cells. The conjugates can be used for
CC immune therapy of inflammatory disorders, e.g. psoriasis, responses
CC associated with inflammatory bowel disease (such as Crohn's disease
CC and ulcerative colitis), ischemic reperfusion, adult respiratory
CC distress syndrome, dermatitis, meningitis, encephalitis, uveitis,
CC autoimmune diseases such as rheumatoid arthritis, Sjorgen's
CC syndrome, vasculitis, diseases involving leukocyte diapedesis,
CC central nervous system inflammatory disorder, multiple organ injury
CC syndrome secondary to septicemia or trauma, alcoholic hepatitis,
CC bacterial pneumonia, antigen-antibody complex mediated diseases,
CC inflammations of the lung, including pleurisy, alveolitis,
CC vasculitis, pneumonia, chronic bronchitis, bronchiectasis, and
CC cystic fibrosis. They can also be used in diagnostic applications.
CC Sequence 242 AA;

Query Match 99.7%, Score 1076, DB 1, Length 242;
Best Local Similarity 99.6%, Pred. No. 2, 10-117;
Matches 241: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKKNIAFLASMFVSIINAYADIQMTQSPSSLSASVGDRTITCRSSSLVHGIGNTY 60
QY 1 MKKNIAFLASMFVSIINAYADIQMTQSPSSLSASVGDRTITCRSSSLVHGIGNTY 60
Db 61 LHWYQKPKAPKLLIYKVSNPFSGVSPFSGSGSGDTFTLTSSLPQEPFATYVCSQT 120
QY 61 LHWYQKPKAPKLLIYKVSNPFSGVSPFSGSGSGDTFTLTSSLPQEPFATYVCSQT 120
Db 121 HVPLIFGGGQTKVEIKRTVAAPSVFIAPPDEQLKSGTASVCLLNINFPYPRKQVQKVDN 180
QY 121 HVPLIFGGGQTKVEIKRTVAAPSVFIAPPDEQLKSGTASVCLLNINFPYPRKQVQKVDN 180
Db 181 ALQSGNSQESVTEQDSKDTYSLSSTLTLSKADYEKKHVYACEVTHQGLSSPVTKSFNFG 240
QY 181 ALQSGNSQESVTEQDSKDTYSLSSTLTLSKADYEKKHVYACEVTHQGLSSPVTKSFNFG 240
241 EC 242
241 EC 242

RESULT 2
ID W69313 standard; Protein: 242 AA.
AC W69313;

DE 15-FEB-1999 (first entry)
DE Anti-IL-8 humanised antibody 664V11M35A.F(ab')2.
KW Humanised antibody; chimeric antibody; monoclonal antibody; mouse;
KW human; Fab; interleukin-8; inflammation; immunotherapy; psoriasis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW ischaemic reperfusion; adult respiratory distress syndrome;
KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;
KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
KW vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;
KW therapy; 664V11M35A.F(ab')2.
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
FH Key Location/Qualifiers
FT CDS 439..1167
FT CD5 /*tag= a
PN W09837200-A2.

PD 27-AUG-1998.
PF 20-FEB-1998: U03337.
PR 22-JAN-1998: US-012115.
PR 21-FEB-1997: US-804444.
PA (GENE) GENENTECH INC.
PI Hsui V. Koumenis I, Leong SP, Presta LP, Shahrokh Z, Sca-9 'A' 15
PI Zapata GA: 21-81
DR WPI: 98-467563/40.
DR N-P8DB; V44953.
PT New conjugates of antibody fragments - having covalently attached
PT non-proteinaceous polymer molecules, particularly polyethylene
PT glycol, for improving the residence time in the circulation.
PS Example K, Fig 4B-D; 328pp; English.
CC This is the amino acid sequence of a polypeptide encoded by
CC plasmid p664V11M35A.F(ab')2 (see V44953) comprising a murine-human
CC chimeric Fab containing complementarity determining regions of
CC murine anti-interleukin-8 (IL-8) monoclonal antibody (MAb) 634.2.5
CC (see W69309-10) in a human template. Humanised anti-IL-8 MABs (see
CC W69301-04) are described for use in diagnostic applications and in
CC the treatment of inflammatory disorders. The invention provides
CC conjugates of an antibody fragment and a polymer, such as PEG, that
CC have improved half-life, mean residence time, and/or clearance rate.
CC The conjugates can be used for immune therapy of e.g. psoriasis,
CC responses associated with inflammatory bowel disease (such as
CC Crohn's disease and ulcerative colitis), ischemic reperfusion,
CC adult respiratory distress syndrome, dermatitis, meningitis,
CC encephalitis, uveitis, autoimmune diseases such as rheumatoid
CC arthritis, Sjorgen's syndrome, vasculitis, diseases involving
CC leukocyte diapedesis, central nervous system inflammatory disorder,
CC multiple organ injury syndrome secondary to septicemia or trauma,
CC alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex
CC mediated diseases, inflammations of the lung, including pleurisy,
CC alveolitis, vasculitis, pneumonia, chronic bronchitis,
CC bronchiectasis, and cystic fibrosis.
SQ Sequence 242 AA;

Query Match 99.6%, Score 1675, DB 1, Length 242;
Best Local Similarity 99.6%, Pred. No. 2, 140-117;
Matches 241: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MKKNIAFLASMFVSIINAYADIQMTQSPSSLSASVGDRTITCRSSSLVHGIGNTY 60
QY 1 MKKNIAFLASMFVSIINAYADIQMTQSPSSLSASVGDRTITCRSSSLVHGIGNTY 60
Db 61 LHWYQKPKAPKLLIYKVSNPFSGVSPFSGSGSGDTFTLTSSLPQEPFATYVCSQT 120
QY 61 LHWYQKPKAPKLLIYKVSNPFSGVSPFSGSGSGDTFTLTSSLPQEPFATYVCSQT 120
Db 121 HVPLIFGGGQTKVEIKRTVAAPSVFIAPPDEQLKSGTASVCLLNINFPYPRKQVQKVDN 180
QY 121 HVPLIFGGGQTKVEIKRTVAAPSVFIAPPDEQLKSGTASVCLLNINFPYPRKQVQKVDN 180
Db 181 ALQSGNSQESVTEQDSKDTYSLSSTLTLSKADYEKKHVYACEVTHQGLSSPVTKSFNFG 240
QY 181 ALQSGNSQESVTEQDSKDTYSLSSTLTLSKADYEKKHVYACEVTHQGLSSPVTKSFNFG 240
241 EC 242
241 EC 242

RESULT 3
ID W69301 standard; Protein: 242 AA.
AC W69301;

DE 15-FEB-1999 (first entry)
DE Humanised anti-IL-8 664.2.5V11M35A light chain.
KW Humanised antibody; monoclonal antibody; interleukin-8;
KW 664.2.5; inflammation; immunotherapy; therapy; psoriasis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW ischaemic reperfusion; adult respiratory distress syndrome;
KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;


```

RESULT 11
ID W095622 standard; Protein: 237 AA.
AC W095622
DE 08-JUN-1999 (first entry)
DE PS1130 expression cassette encoded rhumab cd18 light chain
DE W095622 antibody heavy chain, humanized; myocardial infarction;
KW Burns; thermal injury; ischemic shock; ischaemic haemorrhagic;
KW haemorrhagic; stroke; light chain
OS Mus musculus.
OS Synthetic.
FH Key Location/Qualifiers
FT S1g peptide 1..23
PN W095622
PD 17-DEC-1998.
PE 12-JUN-1999: 012209.
PR 13-JUN-1997: US-874897.
PA (GETH) GENENTECH INC.
DR Wang XM, Oeswein JO, Ongpipattanakul B, Shahrokh Z,
Wang SX, Weissburg RP, Wong RL;
WPI: 99-083866/07.
PT New stable aqueous antibody formulations - comprising an antibody
PT not subjected to lyophilisation, a buffer maintaining the pH at 4.5
PI - 5, a surfactant and a polyol
PS Disclosure: Fig 21A; 87pp; English.
CC The sequence is that of the PS1130 encoded light chain of a humanized
CC murine anti-CD18 antibody rhumab CD18. It can be used for the treatment
CC of disorders which include haemorrhagic shock, thermal injury (such
CC as that resulting from burns), stroke (including ischaemic and
CC haemorrhagic stroke) and myocardial infarction. The antibody
CC formulation can be stabilised at a temperature of 2-8 deg. C
CC for at least one year or at a temperature of 30 deg. C for at
CC least one month and is stable following freezing and thawing.
SQ Sequence 237 AA;

Query Match 87.0%; Score 1462; DB 1; Length 237;
Best Local Similarity 90.9%; Pred. No. 8.63e-101;
Matches 220; Conservative 6; Mismatches 11; Idels 5; Gaps 2;

Db 1 MKKNIAPLLASMEVFSTATNAYADIOMTQSPSSLSASVGDRTVITCRASQD---INN-Y 55
QY 1 MKKNIAPLLASMEVFSTATNAYADIOMTQSPSSLSASVGDRTVITCRASQDVGIGET 60
Db 56 LNWYQKPKAPKLLIYVTSILHSGVSPFSGSGSTCYTLTIISLQEPFATYVQCGN 115
QY 61 LHWYQKPKAPKLLIYVTSILHSGVSPFSGSGSTCYTLTIISLQEPFATYVQCGN 120
Db 115 TLPTTFGGTGKVEIKRTVAAPSVFIPTSPDEQLKSGTASVCLNNFYPEAKVQKVDN 175
QY 121 HVPLTFGGTGKVEIKRTVAAPSVFIPTSPDEQLKSGTASVCLNNFYPEAKVQKVDN 180
Db 175 ALQSGNSQESVTEQDSKDSYLSLSTLLSKADYKHKVYACEVTHQGLSSPVTKSFNPG 235
QY 181 ALQSGNSQESVTEQDSKDSYLSLSTLLSKADYKHKVYACEVTHQGLSSPVTKSFNPG 240
Db 236 EC 237
QY 241 EC 242

RESULT 12
ID W095634 standard; Protein: 237 AA.
AC W095634
DE 06-APR-1999 (first entry)
DE Recombinant humanised anti-CD18 antibody rhumab CD18 light chain.
DE Recombinant humanised anti-CD18 antibody; rhumab CD18; leucine zipper;
KW murine monoclonal antibody; muMAB H52; protein recovery; filtration;
KW chromatography.
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..23

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FT W09856808-A1. /label= signal
PN 17-DEC-1998.
PE 12-JUN-1998: UL2334.
PR 13-JUN-1997: US-050951.
PA (GETH) GENENTECH INC
PI Blank GS, Narindray DS, Zapata GA;
DR WPI: 99-060267/05.
DR N-PSDB: X03840.
PT New method for recovering polypeptides from cell cultures - by
PT treating with reagent and filtering to remove reagent
PS Example, Fig 4; 43pp; English.
CC A method has been developed for recovering a polypeptide comprising: (a)
CC exposing a composition comprising a polypeptide to a reagent which binds
CC to or modifies the polypeptide, where the reagent is immobilized on a
CC solid phase; and (b) passing the composition through a filter bearing an
CC opposite charge to the reagent so as to remove leached reagent from the
CC composition. The present invention also describes a method for modifying
CC a precursor antibody comprising a leucine zipper by exposing the
CC precursor antibody to a protease immobilized on a solid support so that
CC the protease removes the zipper. The methods can be used to purify
CC proteins from cell cultures. They are especially useful for isolating
CC antibodies. The methods overcome the problem of reagent leakage into the
CC protein as is the case in prior art immobilized modification systems. By
CC using a opposite charge filter the reagent can be excluded from the
CC sample, preventing contamination. The present sequence represents the
CC recombinant humanised anti-CD18 antibody (rhMAB CD18) light chain,
CC which is used in an example from the present invention.
SQ Sequence 237 AA;

Query Match 87.0%; Score 1462; DB 1; Length 237;
Best Local Similarity 90.9%; Pred. No. 8.63e-101;
Matches 220; Conservative 6; Mismatches 11; Idels 5; Gaps 2;

Db 1 MKKNIAPLLASMEVFSTATNAYADIOMTQSPSSLSASVGDRTVITCRASQD---INN-Y 55
QY 1 MKKNIAPLLASMEVFSTATNAYADIOMTQSPSSLSASVGDRTVITCRASQDVGIGET 60
Db 56 LNWYQKPKAPKLLIYVTSILHSGVSPFSGSGSTCYTLTIISLQEPFATYVQCGN 115
QY 61 LHWYQKPKAPKLLIYVTSILHSGVSPFSGSGSTCYTLTIISLQEPFATYVQCGN 120
Db 115 TLPTTFGGTGKVEIKRTVAAPSVFIPTSPDEQLKSGTASVCLNNFYPEAKVQKVDN 175
QY 121 HVPLTFGGTGKVEIKRTVAAPSVFIPTSPDEQLKSGTASVCLNNFYPEAKVQKVDN 180
Db 175 ALQSGNSQESVTEQDSKDSYLSLSTLLSKADYKHKVYACEVTHQGLSSPVTKSFNPG 235
QY 181 ALQSGNSQESVTEQDSKDSYLSLSTLLSKADYKHKVYACEVTHQGLSSPVTKSFNPG 240
Db 236 EC 237
QY 241 EC 242

RESULT 13
ID W070703 standard; Protein: 237 AA.
AC W070703;
DE 27-JAN-1999 (first entry)
DE Protein encoded by Fab-display antibody vector pMB4-19-1.6.
DE Murine; humanised antibody; VEGF-induced angiogenesis; tumour;
KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
KW retinal disorder; age-related macular degeneration; diabetic retinopathy;
KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
OS Synthetic.
PN W0945311-A2.
PD 15-OCT-1998.
PE 03-APP-1998: 006604.
PR 06-AUG-1997: US-908469.
PR 07-APR-1997: US-833504.
PA (GETH) GENENTECH INC.
PI Baca M, Chen YM, Lowman HB, Presta LG, Wells JA;
DR WPI: 98-568337/48.

```


CC	TELEX: 910/371-7168
CC	INFORMATION FOR SEQ ID NO. 56:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 242 amino acids
CC	TYPE: Amino Acid
CC	TOPOLOGY: Linear
SC	SEQUENCE 242 AA, 25430 MW, 332270 CN;
	Query Match: 89.9%; Score 1511; DB 2; Length 242;
	Best Local Similarity 87.6%; Pred. No. 2,426-98;
	Mismatches 212; Conservative 18; Indels 0; Gaps 0;
DB	1 MKKNIAPFLASMEVFSTIATNAYADIVMTQTPSLVSLGDOASISCPSSQSLVHGIGNTY 60
QY	1 MKKNIAPFLASMEVFSTIATNAYADIVMTQTPSLVSLGDOASISCPSSQSLVHGIGETY 60
DB	61 LHWLCKFGSGPKLLIKVKNPFSGVFDPFSGSSTFTPLIPSPFAEMGLYFCQSST 120
QY	61 LHWLCKFGSGPKLLIKVKNPFSGVFDPFSGSSTFTPLIPSPFAEMGLYFCQSST 120
DB	121 HVPLTFOAGTKLEKPAAAPTVEIFPPSSSEQLKSGTASVVCILNNYPPEAKVKQVDN 180
QY	121 HVPLTFOAGTKLEKPAAAPTVEIFPPSSSEQLKSGTASVVCILNNYPPEAKVKQVDN 180
DB	181 ALQSGNSGVETQDSKDTYSLSLTLSLKADYEKKHYACVETHOGLSPVTKSFNRG 240
QY	181 ALQSGNSGVETQDSKDTYSLSLTLSLKADYEKKHYACVETHOGLSPVTKSFNRG 240
DE	SEQUENCE 56, Application US/08398612A
XX	Sequence 56, Application US/08398612A
XX	Patent No. 5686070
CC	GENERAL INFORMATION:
CC	APPLICANT: Doershuk, Claire M.
CC	APPLICANT: Fong, Sherman
CC	APPLICANT: Hebert, Caroline Alice
CC	APPLICANT: Kim, Kyung Jin
CC	APPLICANT: Leong, Steven R.
CC	TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory Disorders
CC	NUMBER OF SEQUENCES: 58
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: Genentech, Inc.
CC	STREET: 460 Point San Bruno Blvd
CC	CITY: South San Francisco
CC	STATE: California
CC	COUNTRY: USA
CC	ZIP: 94080
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: MicPatIn (Genentech)
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/08/398,612A
CC	FILING DATE: 01-MAR-1995
CC	CLASSIFICATION: 424
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: 08/398611
CC	FILING DATE: 01-MAR-1995
CC	APPLICATION NUMBER: 08/398612

CC	FILING DATE: 03-MAR-1994
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Love, Richard B.
CC	REGISTRATION NUMBER: 34,650
CC	REFERENCE/DOCKET NUMBER: P0874P1
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: 415/225-5530
CC	TELEFAX: 415/952-9881
CC	TELEX: 910/371-7168
CC	INFORMATION FOR SEQ ID NO. 56:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 242 amino acids
CC	TYPE: Amino Acid
CC	TOPOLOGY: Linear
SC	SEQUENCE 242 AA, 25430 MW, 332270 CN;
	Query Match: 89.9%; Score 1511; DB 1; Length 242;
	Best Local Similarity 87.6%; Pred. No. 2,426-98;
	Mismatches 212; Conservative 18; Indels 0; Gaps 0;
DB	1 MKKNIAPFLASMEVFSTIATNAYADIVMTQTPSLVSLGDOASISCPSSQSLVHGIGNTY 60
QY	1 MKKNIAPFLASMEVFSTIATNAYADIVMTQTPSLVSLGDOASISCPSSQSLVHGIGETY 60
DB	61 LHWLCKFGSGPKLLIKVKNPFSGVFDPFSGSSTFTPLIPSPFAEMGLYFCQSST 120
QY	61 LHWLCKFGSGPKLLIKVKNPFSGVFDPFSGSSTFTPLIPSPFAEMGLYFCQSST 120
DB	121 HVPLTFOAGTKLEKPAAAPTVEIFPPSSSEQLKSGTASVVCILNNYPPEAKVKQVDN 180
QY	121 HVPLTFOAGTKLEKPAAAPTVEIFPPSSSEQLKSGTASVVCILNNYPPEAKVKQVDN 180
DB	181 ALQSGNSGVETQDSKDTYSLSLTLSLKADYEKKHYACVETHOGLSPVTKSFNRG 240
QY	181 ALQSGNSGVETQDSKDTYSLSLTLSLKADYEKKHYACVETHOGLSPVTKSFNRG 240
DE	SEQUENCE 56, Application US/08398613A
XX	Sequence 56, Application US/08398613A
XX	Patent No. 5677426
CC	GENERAL INFORMATION:
CC	APPLICANT: Fong, Sherman
CC	APPLICANT: Hebert, Caroline Alice
CC	APPLICANT: Kim, Kyung Jin
CC	APPLICANT: Leong, Steven R.
CC	TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory Disorders
CC	NUMBER OF SEQUENCES: 58
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: Genentech, Inc.
CC	STREET: 460 Point San Bruno Blvd
CC	CITY: South San Francisco
CC	STATE: California
CC	COUNTRY: USA
CC	ZIP: 94080
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC	OPERATING SYSTEM: IBM PC compatible
CC	SOFTWARE: patin (Genentech)
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/08/398,613A
CC	FILING DATE: 03-MAR-1994

CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WinPatIn (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/98/463.587A
CC FILING DATE: 05-Jun-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 06/050058
CC FILING DATE: 30-APR-1993
CC
CC APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US91/09133
CC FILING DATE: 03-DEC-1991
CC
CC APPLICATION DATA:
CC APPLICATION NUMBER: 07/743614
CC FILING DATE: 09-AUG-1991
CC
CC APPLICATION DATA:
CC APPLICATION NUMBER: 07/715300
CC FILING DATE: 14-JUN-1991
CC
CC APPLICATION DATA:
CC APPLICATION NUMBER: 07/683400
CC FILING DATE: 10-APR-1991
CC
CC APPLICATION DATA:
CC APPLICATION NUMBER: 07/621667
CC FILING DATE: 03-DEC-1990
CC
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Schwartz, Timothy P.
CC REGISTRATION NUMBER: 32171
CC REFERENCE/DOCKET NUMBER: P0645P4D2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-7467
CC TELEFAX: 415/952-9881
CC
CC INFORMATION FOR SEQ ID NO: 25:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 237 amino acids
CC TYPE: Amino Acid
CC TOPOLOGY: Linear
CC
CC SEQUENCE 237 AA; 25977 MW; 322792 CN;
CC
CC Query Match 85.5%; Score 1437; DB 2; Length 237;
CC Best Local Similarity 90.1%; Pred No 5.62e-93;
CC Matches 218; Conservative 5; Mismatches 14; Indels 5; Gaps 3;
CC
Db 1 MKKNIAFLASMEVFSTATNAYADIQMTQSPSSLSASVGDRTVITCRASQD-VN-TAVA- 57
QY 1 MKKNIAFLASMEVFSTATNAYADIQMTQSPSSLSASVGDRTVITCRASQSLVHGIGETY 60
Db 58 --WYQOKPKGKAPKLLIYKVSVPFSGSGSDFTLTITSSLOPEDFATVYCSQST 115
QY 61 LHWYQOKPKGKAPKLLIYKVSVPFSGSGSDFTLTITSSLOPEDFATVYCSQST 120
Db 116 ITPTPTGQGTKEIKPTVAAPSVFIPPPSDEDI KSGTASVVCLLNNFYPPRAKQVQKVDN 175
QY 121 HVPLTEGQGTKEIKPTVAAPSVFIPPPSDEDI KSGTASVVCLLNNFYPPRAKQVQKVDN 180
Db 176 ALQSGNSQSVTEQDSKDSYLSSTLTLSKADYEKKHYACVETHQGLSSPVTKSNRG 235
QY 191 ALQSGNSQSVTEQDSKDSYLSSTLTLSKADYEKKHYACVETHQGLSSPVTKSNRG 240
Db 236 EC 237
QY 241 EC 242

RESULT 6
ID PCT-US91-09133-26 STANDARD PPT 237 AA.
XX AC xxxxxx
XX DT
XX
Sequence 26. Application PC/TUS9109133
XX
Sequence 26. Application PC/TUS9109133
CC GENERAL INFORMATION:
CC APPLICANT: Genentech, Inc.
CC APPLICANT: Garrard, Lisa J.
CC APPLICANT: Henner, Dennis J.
CC APPLICANT: Bass, Steven
CC APPLICANT: Greene, Ronald
CC APPLICANT: Lowman, Henry B.
CC APPLICANT: Wells, James A.
CC APPLICANT: Mathews, David J.
CC TITLE OF INVENTION: Enrichment Method For Variant Proteins
CC TITLE OF INVENTION: With Altered Binding Properties
CC NUMBER OF SEQUENCES: 27
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US91/09133
CC FILING DATE: 19911203
CC
CC CLASSIFICATION: 425
CC PRIOR APPLICATION DATA: 07/743614
CC APPLICATION NUMBER:
CC PRIOR APPLICATION DATA: 07/715300
CC APPLICATION NUMBER:
CC PRIOR APPLICATION DATA: 07/683400
CC APPLICATION NUMBER:
CC APPLICATION NUMBER: 07/621667
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Benson, Robert H.
CC REGISTRATION NUMBER: 30,446
CC REFERENCE/DOCKET NUMBER: 645P4
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/266-1489
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 26:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 237 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC SEQUENCE 237 AA; 25977 MW; 322792 CN;
CC
Query Match 85.5%; Score 1437; DB 3; Length 237;
Best Local Similarity 90.1%; Pred No 5.62e-93;
Matches 218; Conservative 5; Mismatches 14; Indels 5; Gaps 3;
Db 1 MKKNIAFLASMEVFSTATNAYADIQMTQSPSSLSASVGDRTVITCRASQD-VN-TAVA- 57
QY 1 MKKNIAFLASMEVFSTATNAYADIQMTQSPSSLSASVGDRTVITCRASQSLVHGIGETY 60
Db 58 --WYQOKPKGKAPKLLIYKVSVPFSGSGSDFTLTITSSLOPEDFATVYCSQST 115
QY 61 LHWYQOKPKGKAPKLLIYKVSVPFSGSGSDFTLTITSSLOPEDFATVYCSQST 120

CC REFERENCE/DOCKET NUMBER: F1123
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 650/225-1489
 CC TELEFAX: 650/952-9881
 CC INFORMATION FOR SEQ ID NO: 17:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 218 amino acids
 CC TYPE: Amino Acid
 CC TOPOLOGY: Linear
 CC SEQUENCE 219 AA: 23800 MW: 271009 CN:
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 CC Query Match 80.3% Score 1350 DB 2: Length 218:
 CC Best Local Similarity 90.9% Pred No 1: 136-96;
 CC Matches 199: Conservative 5: Mismatches 13: Indels 1: Gaps 1:
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 CC 1 DIQLTQSPSSLSASVGDPTVTITCPASKP-VQGGEGDSVLYNWQCKPKAPKLLIYAASYLE 59
 CC 24 DIQMTQSPSSLSASVGDPTVTITCPSSQSLVHVGIGETYLHWQCKPKAPKLLIYVVSNP 83
 CC 60 SGVPSRFGSGSGSDTDLTISSLPQDFATYVQCSQSHEDPYTFGGQTKVEIKRTVAAPSV 119
 CC 84 SGVPSRFGSGSGSDTDLTISSLPQDFATYVQCSQSHEDPYTFGGQTKVEIKRTVAAPSV 143
 CC 120 FIFPSSDEQLKSTASVWLLNNFYPPKAVQKVKVNAIQQNSQSVTEQDSKSTYSYL 179
 CC 144 FIFPSSDEQLKSTASVWLLNNFYPPKAVQKVKVNAIQQNSQSVTEQDSKSTYSYL 203
 CC 180 SSTLTLSKADYKHKVYACEVTHQGLSSPVTIKSPNREGC 218
 CC 204 SSTLTLSKADYKHKVYACEVTHQGLSSPVTIKSPNREGC 242
 CC
 CC RESULT 9
 CC ID US-09-987-352P-19 STANDARD: PPT: 218 AA
 CC XX XXXXXX
 CC
 CC Sequence 19 Application US/09887352P
 CC Sequence 19, Application US/09887352P
 CC Patent No. 5994511
 CC GENERAL INFORMATION:
 CC APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 CC TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
 CC TITLE OF INVENTION: Improving Polypeptides
 CC NUMBER OF SEQUENCES: 26
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Genentech, Inc.
 CC STREET: 1 DNA Way
 CC CITY: South San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94080
 CC
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: WinPatIn (Genentech)
 CC CURRENT APPLICATION DATA: US/09/987,352P
 CC APPLICATION NUMBER: 09/09887352P
 CC FILING DATE: 03-Jul-1997
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Svoboda, Craig G.
 CC REGISTRATION NUMBER: 39,044
 CC REFERENCE/DOCKET NUMBER: F1123
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 650/225-1489
 CC TELEFAX: 650/952-9881
 CC INFORMATION FOR SEQ ID NO: 19:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 218 amino acids
 CC TYPE: Amino Acid
 CC TOPOLOGY: Linear
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:
 CC
 CC Query Match 80.3% Score 1350 DB 2: Length 218:

CC LENGTH: 218 amino acids
 CC TYPE: Amino Acid
 CC TOPOLOGY: Linear
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:
 CC
 CC Query Match 80.3% Score 1350 DB 2: Length 218:
 CC Best Local Similarity 90.9% Pred No 1: 136-96;
 CC Matches 199: Conservative 5: Mismatches 13: Indels 1: Gaps 1:
 CC
 CC 1 DIQLTQSPSSLSASVGDPTVTITCPASKP-VQGGEGDSVLYNWQCKPKAPKLLIYAASYLE 59
 CC 24 DIQMTQSPSSLSASVGDPTVTITCPSSQSLVHVGIGETYLHWQCKPKAPKLLIYVVSNP 83
 CC 60 SGVPSRFGSGSGSDTDLTISSLPQDFATYVQCSQSHEDPYTFGGQTKVEIKRTVAAPSV 119
 CC 84 SGVPSRFGSGSGSDTDLTISSLPQDFATYVQCSQSHEDPYTFGGQTKVEIKRTVAAPSV 143
 CC 120 FIFPSSDEQLKSTASVWLLNNFYPPKAVQKVKVNAIQQNSQSVTEQDSKSTYSYL 179
 CC 144 FIFPSSDEQLKSTASVWLLNNFYPPKAVQKVKVNAIQQNSQSVTEQDSKSTYSYL 203
 CC 180 SSTLTLSKADYKHKVYACEVTHQGLSSPVTIKSPNREGC 218
 CC 204 SSTLTLSKADYKHKVYACEVTHQGLSSPVTIKSPNREGC 242
 CC
 CC RESULT 10
 CC ID US-09-987-352B-24 STANDARD: PPT: 218 AA
 CC XX XXXXXX
 CC
 CC Sequence 24 Application US/09887352B
 CC Sequence 24, Application US/09887352B
 CC Patent No. 5994511
 CC GENERAL INFORMATION:
 CC APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 CC TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
 CC TITLE OF INVENTION: Improving Polypeptides
 CC NUMBER OF SEQUENCES: 26
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Genentech, Inc.
 CC STREET: 1 DNA Way
 CC CITY: South San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94080
 CC
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: WinPatIn (Genentech)
 CC CURRENT APPLICATION DATA: US/09/887,352B
 CC APPLICATION NUMBER: US/09/887,352B
 CC FILING DATE: 03-Jul-1997
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Svoboda, Craig G.
 CC REGISTRATION NUMBER: 39,044
 CC REFERENCE/DOCKET NUMBER: F1123
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 650/225-1489
 CC TELEFAX: 650/952-9881
 CC INFORMATION FOR SEQ ID NO: 24:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 218 amino acids
 CC TYPE: Amino Acid
 CC TOPOLOGY: Linear
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:
 CC
 CC Query Match 80.3% Score 1350 DB 2: Length 218:

QY 24 DIRMSPSSLSASVGVTLNNFYFPEAKVQKVDNALQSNQSOESVTEQDSKSTYSL 119
 DB 60 SGVPSH#S5SSS5GIDFILLISSQFPEATYVQKSHFVW1GGQSTVEIKRIVAAPSV 113
 QY 84 SGVPSH#S5SSS5GIDFILLISSQFPEATYVQKSHFVW1GGQSTVEIKRIVAAPSV 143
 DB 120 FIFPDSQKSGTASVCLNNFYFPEAKVQKVDNALQSNQSOESVTEQDSKSTYSL 179
 QY 144 FIFPDSQKSGTASVCLNNFYFPEAKVQKVDNALQSNQSOESVTEQDSKSTYSL 203
 DB 180 SSTLSKADYKHKVYACVTHQGLSSPVTYSPNPGE 218
 QY 204 SSTLSKADYKHKVYACVTHQGLSSPVTYSPNPGE 242

RESULT 13
 ID US-08-887 352B-13 STANDARD: PRT: 218 AA

AC XXXXXX

DT

DE Sequence 13, Application US/08587352B

CC Sequence 13, Application US/08587352B

CC Patent No. 5994511

CC GENERAL INFORMATION:

CC APPLICANT: Henry B. Lowman, Leonard G. Prosta, Paula M. Jardieu, John Lowe

CC TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of

CC TITLE OF INVENTION: Improving Polypeptides

CC NUMBER OF SEQUENCES: 26

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Genentech, Inc.

CC STREET: 1 DNA Way

CC CITY: South San Francisco

CC STATE: California

CC COUNTRY: USA

CC ZIP: 94080

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Winpatin (Genentech)

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/087352B

CC FILING DATE: 03-Jul-1997

CC CLASSIFICATION: 530

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Svoboda, Craig G.

CC REGISTRATION NUMBER: 39,044

CC REFERENCE/DOCKET NUMBER: F1123

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 650/225-1489

CC TELEFAX: 650/952-9881

CC INFORMATION FOR SEQ ID NO. 13:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 218 amino acids

CC TYPE: Amino Acid

CC TOPOLOGY: Linear

CC SEQUENCE 218 AA: 23550 MW: 271154.2N.

Query Match 79.8%; Score 1342; DB 2; Length 218;

Best Local Similarity 90.4%; Pred. No. 4 288-88;

Matches 198; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

DB 1 DQIQLSPSSLSASVGVTLNNFYFPEAKVQKSHFVW1GGQSTVEIKRIVAAPSV 59

QY 24 DIRMSPSSLSASVGVTLNNFYFPEAKVQKVDNALQSNQSOESVTEQDSKSTYSL 83

DB 60 SGVPSH#S5SSS5GIDFILLISSQFPEATYVQKSHFVW1GGQSTVEIKRIVAAPSV 119

QY 84 SGVPSH#S5SSS5GIDFILLISSQFPEATYVQKSHFVW1GGQSTVEIKRIVAAPSV 143

QY 120 FIFPDSQKSGTASVCLNNFYFPEAKVQKVDNALQSNQSOESVTEQDSKSTYSL 179
 QY 144 FIFPDSQKSGTASVCLNNFYFPEAKVQKVDNALQSNQSOESVTEQDSKSTYSL 203
 DB 180 SSTLSKADYKHKVYACVTHQGLSSPVTYSPNPGE 218
 QY 204 SSTLSKADYKHKVYACVTHQGLSSPVTYSPNPGE 242

RESULT 14
 ID US-08-491-334A-28 STANDARD: PRT: 237 AA.

AC XXXXXX

DT

DE Sequence 28, Application US/08491334A

CC Sequence 28, Application US/08491334A

CC Patent No. 5874080

CC GENERAL INFORMATION:

CC APPLICANT: Hebert, Caroline A.

CC APPLICANT: Kabakoff, Phona C

CC APPLICANT: Moore, Mark W.

CC TITLE OF INVENTION:

CC TITLE OF INVENTION: Agents for Treatment of Inflammatory

CC NUMBER OF SEQUENCES: 58

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Genentech, Inc.

CC STREET: 450 Point San Bruno Blvd

CC CITY: South San Francisco

CC STATE: California

CC COUNTRY: USA

CC ZIP: 94080

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Winpatin (Genentech)

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/491,334A

CC FILING DATE: 27-Jun-1995

CC CLASSIFICATION: 424

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/398611

CC FILING DATE: 01-MAR-1995

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/205864

CC FILING DATE: 03-MAR-1994

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Love, Richard P.

CC REGISTRATION NUMBER: 34,659

CC REFERENCE/DOCKET NUMBER: P0874P2

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 415/225-5530

CC TELEFAX: 415/952-9881

CC TELEX: 910/371-7168

CC INFORMATION FOR SEQ ID NO. 28:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 237 amino acids

CC TYPE: Amino Acid

CC TOPOLOGY: Linear

CC SEQUENCE 237 AA: 26087 MW: 317916.6N.

Query Match 79.7%; Score 1340; DB 2; Length 237;

Best Local Similarity 81.8%; Pred. No. 5,97e-86;

Matches 198; Conservative 19; Mismatches 20; Indels 5; Gaps 3;

DB 1 MKKNTAFLLASNFESINAYADIVMTQSKFMSTSVGDPVSVTKASON-V--G-TN 55

QY 1 MKKNTAFLLASNFESINAYADIVMTQSKFMSTSVGDPVSVTKASON-V--G-TN 55




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#authors      Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata,
               F.; Yamaki, S.; Kazi, H.; Takashi, I.; Shinoda, T.
#submission   submitted to JIPID, November 1998
#description   A new subgroup of kappa type light chains (Vkv) identified in
               cases of AL amyloidosis.
#accession    JE0243
#molecule_type protein
#residues     1-215 #label ALI
SUMMARY       #length 215 #molecular-weight 23463 #checksum 78

Query Match      72.8%; Score 1224; DB 2; Length 215;
Best Local Similarity 82.3%; Pred. No. 7.47e-173;
Matches 181; Conservative 18; Mismatches 15; Indels 6; Gaps 4;

Db 1 FVMTQSPATLSVSPGERATLISGASQSVHS--N--LAWYQKPKQCAPLLIYRASTRA 55
QY 24 DIQMTQSPSSLSASVDGVITTCPSQSLSVHGIGETYLHWYQKPKGKAPKLLIYKVSNEF 83
56 LQIPAFSSGSGSIDFILLISLSSEAFALYVQYQNTNPTLPGQGTQVETKPTVAAPS 115
QY 24 DIQMTQSPSSLSASVDGVITTCPSQSLSVHGIGETYLHWYQKPKGKAPKLLIYKVSNEF 83
84 SGVPSRFSGSGSGTDFTLTIISLQPEDFAFYCSQTHVPLTFGGGTQVETKPTVAAPS 142
116 VFIPPSDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 175
QY 143 FIPPSDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 202
176 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 215
QY 203 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 242

RESULT 3
ENTRY    JE0243 #type complete
TITLE    Ig kappa chain NTG93 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change
ACCESSIONS
REFERENCE JE0243
#authors  Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata,
           F.; Yamaki, S.; Kazi, H.; Takashi, I.; Shinoda, T.
#submission submitted to JIPID, November 1998
#description A new subgroup of kappa type light chains (Vkv) identified in
           cases of AL amyloidosis.
#accession JE0243
#molecule_type protein
#residues 1-215 #label ALI
SUMMARY   #length 215 #molecular-weight 23455 #checksum 9947

Query Match      70.3%; Score 1181; DB 2; Length 215;
Best Local Similarity 80.5%; Pred. No. 8.37e-166;
Matches 177; Conservative 17; Mismatches 20; Indels 6; Gaps 6;

Db 1 FVMTQSPATLSVSPGERATLISGASQSV--AT--NV--V--WYMQKLGQAPLLIYDASTRA 55
QY 24 DIQMTQSPSSLSASVDGVITTCPSQSLSVHGIGETYLHWYQKPKGKAPKLLIYKVSNEF 83
56 LQIPAFSSGSGSIDFILLISLSSEAFALYVQYQNTNPTLPGQGTQVETKPTVAAPS 115
QY 84 SGVPSRFSGSGSGTDFTLTIISLQPEDFAFYCSQTHVPLTFGGGTQVETKPTVAAPS 142
116 VFIPPSDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 175
QY 143 VFIPPSDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 202
176 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 215
QY 203 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 242

RESULT 4
ENTRY    A23746 #type complete
TITLE    Ig kappa chain V-III (KAL cold agglutinin) - human

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ORGANISM #formal_name Homo sapiens #common_name man
DATE      30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change
16-Aug-1996
ACCESSIONS A23746
REFERENCE   A23746
#authors   Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
#journal   J. Biol. Chem. (1991) 266:2936-2942
#title     The primary structure of the Fab fragment of protein KAU, a
           monoclonal immunoglobulin M cold agglutinin.
#cross-references MIMD:91131575
#accession A23746
#status     preliminary
#molecule_type protein
#residues 1-215 #label LEO
KEYWORDS   heterotrimer; immunoglobulin
SUMMARY    #length 215 #molecular-weight 23050 #checksum 116

Query Match      67.8%; Score 1140; DB 2; Length 215;
Best Local Similarity 80.3%; Pred. No. 4.31e-159;
Matches 175; Conservative 16; Mismatches 13; Indels 4; Gaps 4;

Db 1 EIVLTQSPATLSLSPGERATLISGASQSV-S--SN--YLAWYQKPKQCAPLLIYDASSRA 56
QY 24 DIQMTQSPSSLSASVDGVITTCPSQSLSVHGIGETYLHWYQKPKGKAPKLLIYKVSNEF 83
57 TGIPTDFSGSGSDTDLTILSLRLEPEDFAFYVQYQYGGSSPLIFGGGTQVETKRTVAAPS 116
QY 84 SGVPSRFSGSGSGIDFILLISLQPEDFAFYCSQTHVPLTFGGGTQVETKRTVAAPS 143
117 FIPPSDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 176
QY 144 FIPPSDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 203
177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 214
QY 204 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 241

RESULT 5
ENTRY    JE0241 #type complete
TITLE    Ig kappa chain AM37 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change
05-Dec-1998
ACCESSIONS JE0241
REFERENCE   JE0241
#authors   Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima,
           M.; Takashi, I.; Shinoda, T.
#submission submitted to JIPID, November 1998
#description Structure relationship of kappa type light chains with AL
           amyloidosis: Multiple deletions found in a Vkv protein
#accession JE0241
#molecule_type protein
#residues 1-216 #label ALI
SUMMARY    #length 216 #molecular-weight 23926 #checksum 4962

Query Match      67.3%; Score 1132; DB 2; Length 216;
Best Local Similarity 77.2%; Pred. No. 8.78e-158;
Matches 159; Conservative 15; Mismatches 32; Indels 3; Gaps 3;

Db 1 DIVLTQSPDPLAVSLGERATINCKSSQSVLYN--SKNFLAWYQKPKGQ--PKLLIW--ANVPE 57
QY 24 DIQMTQSPSSLSASVDGVITTCPSQSLSVHGIGETYLHWYQKPKGKAPKLLIYKVSNEF 83
58 SGVPSRFSGSGSIDFILLISNLQAEFLVAVYQYQYVSTPSFGGGRLKRTVAAPS 117
QY 84 SGVPSRFSGSGSGSIDFILLISLQPELFAFYCS--HVPILFGGTQVETKRTVAAPS 143
118 FIPPSDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 177
QY 144 FIPPSDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 203
178 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 216

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RC NEW YORK (1969).
 RP [6]
 RP SEQUENCE (BENCE-JONES PROTEIN CUM)
 RX MEDLINE: 68242259.
 RA Hilschmann N.F.
 RE "The complete amino acid sequence of Bence Jones protein Gm (Kappa type)."
 RI Hilschmann N.F. Physiol Chem 248:1718-1722(1967).
 RC Hilschmann N.F. Physiol Chem 248:1718-1722(1967).
 RN [7]
 RP SEQUENCE (BENCE-JONES PROTEIN AG)
 RX MEDLINE: 68234734.
 RA Titani K., Shinoda T., Putnam F.W.
 RE "The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges."
 RI J. Biol. Chem. 244:3650-3660(1969).
 RN [8]
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN CH)
 RX MEDLINE: 70201507.
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.
 RE "Macroglobulin structure. Variable sequence of light and heavy chains."
 RI Science 169:56-59(1970).
 RL Science 169:56-59(1970).
 CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER.
 CC 45-ALA & 83-VAL: THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC MARKER, 45-ALA AND 83-LEU.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its context is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J00241; AAA58989.1;
 DR EMBL: V00557; CAA23923.1;
 DR PIR: A02116; K3HU.
 DR MIM: 147200;
 DR PROSITE: PS00099; IG_MHC; 1.
 DR PFAM: PF00047; Ig: 1.
 KW Immunoglobulin domain; immunoglobulin C region
 FT NON_TER 1
 FT DISULFID 26 86
 FT DISULFID 106 106
 FT VARIANT 83 83
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT V->L (IN INV(1,2) MARKER).
 FT /FTID=VAR_003897.
 FT D->N (IN REF. 7 AND 8).
 FT E->Q (IN REF. 5 AND 6).
 FT CONFLICT 14 14
 FT CONFLICT 57 57
 SEQUENCE 106 AA; 11609 MW; 51984D1FDD3722E8 CRC64;
 Query Match 42.9%; Score 721; DB 1; Length 106.
 Best Local Similarity 100.0%; Pred No 1 54e-145.
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DE 1 TVAAKSVITFTSCQLSGTAAVLLNNPPEAVVMPVVALSGNSGNSVTFPS 60
 QY 137 TVAAKSVITFTSCQLSGTAAVLLNNPPEAVVMPVVALSGNSGNSVTFPS 196
 DB 51 KTSVLSLSTILSKADYKHKVACEVHGLSSPVTKSPNFGEC 106
 QY 137 KTSVLSLSTILSKADYKHKVACEVHGLSSPVTKSPNFGEC 242
 RESULT 2
 ID KY01.MOUSE STANDARD: FPI: 113 AA
 AC P01631
 DT 21-JUL-1986 (Rel. 01, Created)
 DI 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION 26-10
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE: 83178921
 RA Novotny J., Margolles M.N.
 RE "Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody."
 RI Biochemistry 22:1153-1159(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
 CC PROTEIN THAT BINDS DIGOXIN.
 DR PIR: A01914; KYMS26
 DR PFAM: PF00047; Ig: 1
 KW Immunoglobulin V region; Monoclonal antibody; Hybridoma
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 40 54
 FT COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 55 61
 FT COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT COMPLEMENTARITY-DETERMINING 4.
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON_TER 113 113
 BY SIMILARITY.
 SQ SEQUENCE 113 AA; 12273 MW; P0F99CE949AP4C2A CRC64;
 Query Match 35.9%; Score 602; DB 1; Length 113.
 Best Local Similarity 70.8%; Pred. No. 1.01e-115.
 Matches 80; Conservative 20; Mismatches 13; Indels 0; Gaps 0;
 DE 1 DVMTQPLSLPVSLDQASISGRSSQSLVHSNGNTLYLWYLCFAQCSPTIYVSNPF 40
 QY 24 DIQMTSPSSLSASVGPVITCPSSQSLVHSGEYLVHWYQCKPKAKPLLYKVNPF 83
 DB 51 SGVDPFSSGSGGTFTLKISRVAEELGIYFCSQTHVPTFGSGTKLEIR 113
 QY 84 SGVDPFSSGSGGTFTLKISRVAEELGIYFCSQTHVPTFGSGTKLEIR 136
 RESULT 3
 ID KY1N.HUMAN STANDARD: FPI: 108 AA
 AC P01606;
 DT 21-JUL-1986 (Rel. 01, Created)
 DI 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION 0U.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 70201507.
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.
 RE "Macroglobulin structure: variable sequence of light and heavy chains."
 RI Science 169:56-59(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
 DR PIR: A01872; KIHU01.
 DR HSP: P01607; IPEI
 DR PFAM: PF00047; Ig: 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49
 FT COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 50 56
 FT COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 57 88
 FT COMPLEMENTARITY-DETERMINING 4.
 FT DOMAIN 89 97
 FT COMPLEMENTARITY-DETERMINING 5.
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 BY SIMILARITY.
 SQ SEQUENCE 108 AA; 11777 MW; 82F3D4A241C5827E CRC64;
 Query Match 34.2%; Score 575; DB 1; Length 108;


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RESULT 2
ID QV4V0: PRELIMINARY: PFI: 197 AA.
AC QV4V0:
DI 01-NOV-1999 (Tremblrel. 12, Created)
DI 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DI 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE D576H24.2 (SIPP-BETA1) (SIGNAL REGULATOR PROTEIN BETA 1))
GN D576H24.2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthalia; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MATTHEWS L.J.
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL049634; CAB46661.1; -.
SQ SEQUENCE 397 AA: 43033 MW: 40915 CPO32:
      1358: Score 227, DB 4: Length 397;
      Best Local Similarity 26.6%; Pred No 2 250-24;
      Matches 61, Conservative 63, Mismatches 98, Indels 21, Gaps 20;

DL 12 FELLILLILLGTVAGDELOVIOPEKSVSVAAGESATLPCAMTSLIP-VQPI-M-WEP 69
QY 5 AFLASVFVSIAINAYADIMTSPSSLSASVGEVITICPSSASLVH31SETVLRHY 65
DB 69 G-AG-APPELLIYNQFEGHPPTVVELTKPNKLDPSISNITPADACTYCVKPKFGS 126
QY 66 EKEKAKELLYKVN-RFSGVPSRFSGSGST-IFTLTISSIQEDPATYCSQ-STHPV 122
DL 127 ECVVEVSEATLSEVNFESAV-VSGRAVATPHTVSPFCESHGSPSPPTIKWPN 185
QY 123 P-LTPGCGTVEIK-PTVAAPSVFTTPSDQKSGTASVCLNNPYPPEAKVQW-KV 178
DL 136 UNEL-3-DEFTN-DRAGESVSISHTAPVWLPITQSCQ-V-ICEAHITL 233
QY 179 DNAGQSNQSVSVIEKSDISLSL-SSI-LILSKALAEKHKVACEVTHQL 225

RESULT 3
ID F8324: PRELIMINARY: PFI: 503 AA.
AC F8324: Q00683:
DI 01-NOV-1998 (Tremblrel. 08, Created)
DI 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DI 01-NOV-1998 (Tremblrel. 12, Last annotation update)
DE PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 PRECURSOR
(SHP SUBSTRATE-1) (INHIBITORY RECEPTOR SHPS-1) (SHPS-1) (SIGNAL-
REGULATOR PROTEIN ALPHA-1) (STEP-ALPHA1) (MYD-1 ANTIGEN)
GN PIPN1 OF SHPS-1 OF D5584324.1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthalia; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-BRAIN:
RX MEDLINE: 97222999.
RA YAMA T., HALLCAKI T., AMAN K., MAISUEA Y., IAPAKASHI N., ICHI E.,
PA FUKIYA V., KASUGA M.
RT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
localization of genes."
RL Biochem. Biophys. Res. Commun. 231:61-67(1997)
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=PLACENTA:
RX MEDLINE: 97215901.
RA KUBITONENKV A., CHEN Z., SUPES I., WANG H., SCHILLING T.,
RA ULURICH A.
RT "A family of proteins that inhibit signalling through tyrosine kinase
receptors."
RL Nature 386:181-186(1997)
RN [3]
RP SEQUENCE OF 145-503 FROM N.A.
RA BATES K.

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PL Submitted (MAP-1999) to the EMBL/GenBank/DBJ databases.
DI 01-NOV-1999 (Tremblrel. 12, Created)
DI 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DI 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE 2C (SHP-2) AFTER TYROSINE PHOSPHORYLATION INDUCED BY VARIOUS
MITOGENS AND CELL ADHESION. MAY ACT AS A DOCKING PROTEIN AND
INDUCE TRANSLOCATION OF SHP-2 FROM THE CYTOSOL TO THE PLASMA
MEMBRANE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN BRAIN.
HIGH LEVELS ALSO PRESENT IN HEART, SPLEEN, TESTIS, OVARY AND
PEPTIDEPAL BLOOD LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY CONTAINS
TWO C1-LIKE AND ONE V-LIKE DOMAINS.
DR EMBL: D86043; RAA12974.1; -.
DR EMBL: Y10375; CAA71403.1; -.
DR EMBL: AL034562; CAB38874.1; -.
DR MIM: 602461; -.
DR PFAM: PF00047; Iq: 3
KW Signal: Transmembrane; Alternative splicing; Immunoglobulin domain;
KW Glycoprotein; SH3-binding; Phosphorylation.
PL SIGNAL 1 26
ET CHAIN 27 503
ET DOMAIN 27 372
ET TRANSMEM 373 393
ET DOMAIN 394 503
ET DOMAIN 43 129
ET DOMAIN 164 233
ET DOMAIN 266 339
ET DOMAIN 428 431
ET DOMAIN 438 443
ET DOMAIN 452 455
ET DOMAIN 459 472
ET DOMAIN 495 498
ET MOD_RES 428 428
ET MOD_RES 452 452
ET MOD_RES 459 469
ET MOD_RES 495 495
ET CARBOHYD 244 244
ET CARBOHYD 269 269
ET CARBOHYD 291 291
ET CARBOHYD 318 318
SQ SEQUENCE 503 AA: 54912 MW: 504572F CPO32:
      1358: Score 227, DB 4: Length 503;
      Best Local Similarity 26.6%; Pred No 2 250-24;
      Matches 61, Conservative 57, Mismatches 94, Indels 17, Gaps 17;

DL 17 LLAASCAISVAGR-ERKQVTEKSVSVAAGESAIIHCTVT-SLIF-VQ-P-ICWFRG 71
QY 7 ELASNEFVSIAINAYADIMTSPSSLSASVGEVITICPSSASLVH31SETVLRHY 66
DL 72 -AG-PAPELLIYNQFEGHPPTVVELTKPNKLDPSISNITPADACTYCVKPKFGS 129
QY 67 KFSKAPKLLIYKVN-RFSGVPSRFSGSGST-IFTLTISSIQEDPATYCSQ-STHPV 123
DB 130 DTEKSGAGTELSPAKPSAPV-VSGPAARATPQRTVSFTCESHCFSPPDITIKWFKNGN 188
QY 124 LT-PGQGTVEIK-PTVAAPSVFTTPSDQKSGTASVCLNNPYPPEAKVQW-KVDN 180
DB 189 EL-S-DFQTNV-DPVGESVSYSHSIKAVLTREDVSHVSVICEVAHVTL 234
QY 181 ALQGSNSQSVTEQDSKDSVLSLSTLTLSKADYEKHKVACEVTHQCL 229

RESULT 4
ID Q00241: PRELIMINARY: PFI: 398 AA.
AC Q00241:
DI 01-NOV-1998 (Tremblrel. 08, Created)
DI 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DI 01-AUG-1999 (Tremblrel. 11, Last annotation update)
DE SIGNAL-REGULATOR PROTEIN BETA-1 PRECURSOR (SIPP-BETA1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

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